

REMARKS

Claims 1-40 constitute the pending claims in the present application. Applicants respectfully request reconsideration in view of the following remarks. Issues raised by the Examiner will be addressed below in the order they appear in the prior Office Action.

1-4. Applicants note that the previous amendment was entered and considered, and that claims 1-13 and 23-36 are withdrawn as being directed to a non-elected invention. Applicants will cancel such claims upon indication of allowable subject matter.

5. Applicants note that item BX on the previous IDS was not considered. This item will not be resubmitted.

6. Claims 14-22 and 37-40 are rejected under 35 U.S.C. § 101 because the claimed invention allegedly lacks patentable utility. Applicants respectfully traverse this rejection.

Faye et al., WO 99/07836, cited as reference BV in the IDS filed January 29, 2001, discloses nucleotide and amino acid sequences with strong similarity to SEQ ID Nos. 13 and 14. For example, SEQ ID No. 2 of Faye et al. differs from SEQ ID No. 14 of the present application by merely six amino acids, 98% identity (see sequence comparison attached as Exhibit A). On page 8, lines 30-36, Faye et al. state that cells transformed by a plasmid encoding SEQ ID No. 2 (CaCIV1) rescues *S. cerevisiae* cells which lack a functional ScCIV1 gene, a gene essential for cell viability. Accordingly, an agent which blocks the function of CaCIV1 would be expected to exhibit antifungal activity. Applicants asserted that the claimed subject matter was useful for drug screening assays on page 4, lines 5-6, and page 9, lines 11-18, and Faye et al. demonstrate the accuracy of these assertions.

Moreover, Applicants submit that use as a diagnostic tool, despite the Office Action's assertions to the contrary, is a *specific and substantial* utility that was asserted in the present application. The mere fact that other sequences may also be used for this purpose does not contradict this utility, or make it any less specific. For example, many different compounds have been identified – and patented – as antidepressant pharmaceuticals. The mere fact that *one* antidepressant is known does not make subsequent compounds identified as having similar

activity any less useful, nor their utility any less specific, as the arguments recited in the Office Action suggest. Accordingly, the mere fact that other nucleic acids identified and sequenced from *C. albicans* could be used for diagnostic purposes does not undercut the fact that the presently claimed subject matter could also be used to diagnose the presence of *C. albicans* in a patient. Contrary to the statements in the Office Action, it is not true that *any* nucleic acid would have this utility. This utility is dependent on the particular sequence disclosed by Applicants, and random sequences would typically be ineffective for this purpose. This fact demonstrates that the asserted utility is, in fact, specific.

For the reasons set forth above, Applicants submit that the pending claims fully comply with the requirements of 35 U.S.C. § 101. Reconsideration and withdrawal of this rejection is respectfully requested.

With respect to the rejection of these claims as not being enabled because the claimed invention was not allegedly supported by a utility, Applicants submit that the uses described above were described in the application with sufficient detail and clarity that one of skill in the art could have practiced the claimed invention throughout its scope. Reconsideration and withdrawal of this rejection is respectfully requested.

7. Claims 37-40 are rejected under 35 U.S.C. §112, first paragraph, as allegedly containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention. Applicants respectfully traverse this rejection to the extent it is maintained over the claims as amended.

Applicants have amended claim 37 to more particularly point out conditions recited on page 13 of the application. Reconsideration and withdrawal of this rejection is respectfully requested.

8. Claims 37-40 are rejected under 35 U.S.C. §112, second paragraph, as allegedly being indefinite. Applicants respectfully traverse this rejection to the extent it is maintained over the claims as amended.

Applicants have amended claim 37 as pointed out above. Applicants submit that hybridization is a common laboratory technique, and that one of skill in the art would readily be able to determine whether or not a nucleic acid sequence hybridizes to another under specified conditions. Reconsideration and withdrawal of this rejection is respectfully requested.

CONCLUSION

In view of the foregoing amendments and remarks, Applicants submit that the pending claims are in condition for allowance. Early and favorable reconsideration is respectfully solicited. The Examiner may address any questions raised by this submission to the undersigned at 617-951-7000. Should an extension of time be required, Applicants hereby petition for same and request that the extension fee and any other fee required for timely consideration of this submission be charged to **Deposit Account No. 18-1945**.

Date: July 5, 2001

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Respectfully Submitted,



David P. Halstead
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results of BLAST

BLASTP 2.1.3 [Apr-11-2001]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 992903094-22877-12488

Query=

(339 letters)

Database: pat

71,783 sequences; 10,525,338 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 503 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments

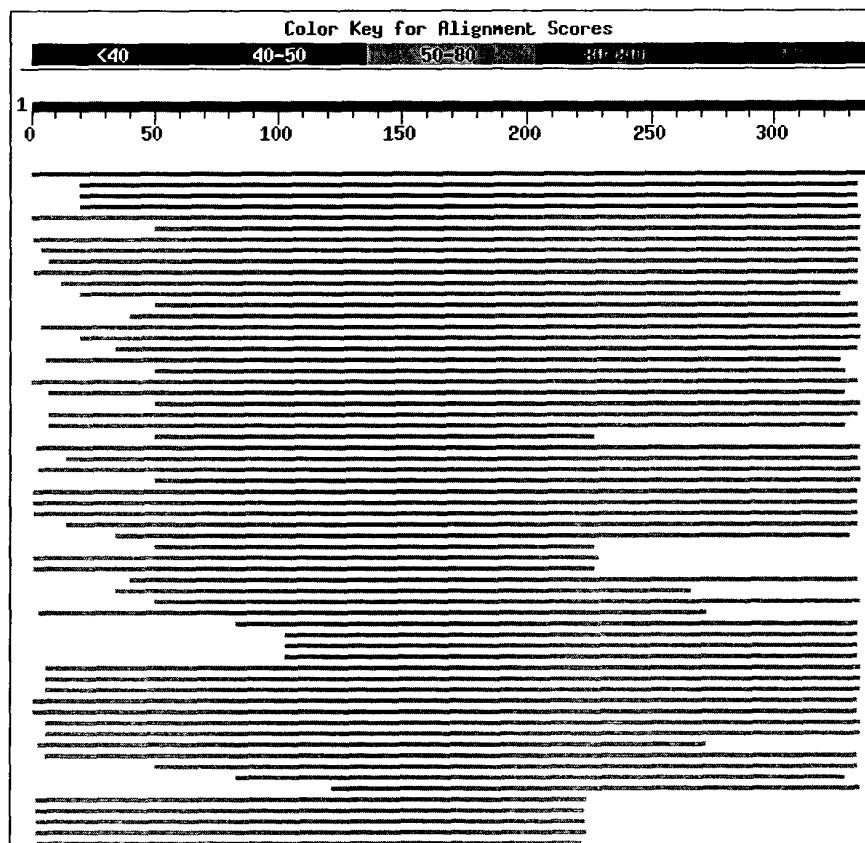


EXHIBIT A

Sequences producing significant alignments:				Score (bits)	E Value
gi	9928920	emb	CAC05182.1	(AX005954) unnamed protein produ...	624 e-179
gi	6733419	emb	CAB69315.1	(A84499) unnamed protein product...	82 4e-16
gi	10061049	gb	AAE37002.1	Sequence 2 from patent US 5986055	82 4e-16
gi	6733417	emb	CAB69314.1	(A84497) unnamed protein product...	82 4e-16
gi	11340555	emb	CAC17042.1	(AX040958) unnamed protein prod...	78 9e-15
gi	12225900	emb	CAC21767.1	(AX048754) unnamed protein prod...	76 4e-14
gi	11340559	emb	CAC17043.1	(AX040962) unnamed protein prod...	74 8e-14
gi	10057862	gb	AAE34768.1	Sequence 5 from patent US 5977442	74 8e-14
gi	2491504	gb	AAB79640.1	I64354 Sequence 2 from patent US 5...	74 1e-13
gi	5950570	gb	AAE04796.1	Sequence 2 from patent US 5869043	73 2e-13
gi	10057864	gb	AAE34770.1	Sequence 7 from patent US 5977442	72 5e-13
gi	10057863	gb	AAE34769.1	Sequence 6 from patent US 5977442	71 7e-13
gi	4001196	gb	AAC94628.1	AR025720 Sequence 20 from patent U...	71 7e-13
gi	10057861	gb	AAE34767.1	Sequence 4 from patent US 5977442	71 1e-12
gi	11340563	emb	CAC17044.1	(AX040966) unnamed protein prod...	70 2e-12
gi	12827408	gb	AAE50558.1	Sequence 17 from patent US 6114517	69 3e-12
gi	1831632	gb	AAB46086.1	Sequence 16 from patent US 559590...	69 3e-12
gi	4001195	gb	AAC94627.1	AR025719 Sequence 19 from patent U...	69 4e-12
gi	12225904	emb	CAC21768.1	(AX048758) unnamed protein prod...	68 6e-12
gi	5955786	gb	AAE07442.1	Sequence 9 from patent US 5801015	68 8e-12
gi	10057859	gb	AAE34765.1	Sequence 2 from patent US 5977442	68 8e-12
gi	10058203	gb	AAE35109.1	Sequence 2 from patent US 5981248	68 9e-12
gi	5955788	gb	AAE07444.1	Sequence 11 from patent US 5801015	67 1e-11
gi	12225908	emb	CAC21769.1	(AX048762) unnamed protein prod...	67 1e-11
gi	10057860	gb	AAE34766.1	Sequence 3 from patent US 5977442	67 2e-11
gi	1831631	gb	AAB46085.1	Sequence 15 from patent US 559590...	66 3e-11
gi	14100016	gb	AAE53156.1	Sequence 24 from patent US 6140124	66 4e-11
gi	1831630	gb	AAB46084.1	Sequence 14 from patent US 559590...	65 5e-11
gi	10058204	gb	AAE35110.1	Sequence 4 from patent US 5981248	65 5e-11
gi	10049308	gb	AAE26215.1	Sequence 2 from patent US 5948885	65 6e-11
gi	5942087	gb	AAE01619.1	Sequence 3 from patent US 5858765	65 6e-11
gi	3997995	gb	AAC91427.1	AR017537 Sequence 14 from patent U...	65 6e-11
gi	6733351	emb	CAB69295.1	(A84431) unnamed protein product...	65 6e-11
gi	6733369	emb	CAB69304.1	(A84449) unnamed protein product...	65 6e-11
gi	10051523	gb	AAE28430.1	Sequence 33 from patent US 5958784	65 7e-11
gi	2491506	gb	AAB79642.1	I64356 Sequence 4 from patent US 5...	64 9e-11
gi	12225892	emb	CAC21765.1	(AX048746) unnamed protein prod...	64 1e-10
gi	1609068	gb	AAB12024.1	Sequence 4 from patent US 5512473...	64 1e-10
gi	10051521	gb	AAE28428.1	Sequence 31 from patent US 5958784	64 1e-10
gi	3715669	emb	CAA03585.1	(A61243) CYCLIN-DEPENDENT KINASE...	64 1e-10
gi	6733343	emb	CAB69291.1	(A84423) unnamed protein product...	63 3e-10
gi	6733361	emb	CAB69300.1	(A84441) unnamed protein product...	63 3e-10
gi	1831627	gb	AAB46081.1	Sequence 11 from patent US 559590...	63 3e-10
gi	1831622	gb	AAB46076.1	Sequence 2 from patent US 5595904...	63 3e-10
gi	14107100	gb	AAE55954.1	Sequence 18 from patent US 6165461	63 3e-10
gi	6733349	emb	CAB69294.1	(A84429) unnamed protein product...	63 4e-10
gi	12827407	gb	AAE50557.1	Sequence 15 from patent US 6114517	63 4e-10
gi	6733367	emb	CAB69303.1	(A84447) unnamed protein product...	63 4e-10
gi	14100017	gb	AAE53157.1	Sequence 46 from patent US 6140124	62 4e-10
gi	2491505	gb	AAB79641.1	I64355 Sequence 3 from patent US 5...	62 4e-10
gi	10188272	emb	CAC09126.1	(AX027295) unnamed protein prod...	62 5e-10
gi	10188270	emb	CAC09125.1	(AX027293) unnamed protein prod...	62 5e-10
gi	5976240	gb	AAE13650.1	Sequence 4 from patent US 5830699...	61 1e-09
gi	10057865	gb	AAE34771.1	Sequence 8 from patent US 5977442	61 1e-09
gi	1252508	gb	AAA93767.1	Sequence 2 from patent US 5459036	61 1e-09
gi	10067610	gb	AAE40373.1	Sequence 8 from patent US 6001580	61 1e-09
gi	10051520	gb	AAE28427.1	Sequence 30 from patent US 5958784	61 1e-09
gi	3012816	gb	AAC11659.1	I76662 Sequence 43 from patent US ...	60 2e-09

gi	10051525	gb	AAE28432.1	Sequence 35 from patent US 5958784	60	2e-09
gi	14103310	gb	AAE54744.1	Sequence 2 from patent US 615341...	59	3e-09
gi	10051519	gb	AAE28426.1	Sequence 29 from patent US 5958784	59	3e-09
gi	12813502	gb	AAE44802.1	Sequence 31 from patent US 6083713	59	4e-09
gi	1831624	gb	AAB46078.1	Sequence 6 from patent US 5595904...	58	7e-09
gi	3997604	gb	AAC91034.1	AR017146 Sequence 6 from patent US...	58	8e-09
gi	1831629	gb	AAB46083.1	Sequence 13 from patent US 559590...	58	8e-09
gi	12225932	emb	CAC21775.1	(AX048786) unnamed protein prod...	58	9e-09
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gi	11340567	emb	CAC17045.1	(AX040970) unnamed protein prod...	58	1e-08
gi	9998363	emb	CAC07562.1	(AX012313) unnamed protein produ...	57	1e-08
gi	5951591	gb	AAE05817.1	Sequence 38 from patent US 586964...	57	2e-08
gi	10057866	gb	AAE34772.1	Sequence 9 from patent US 5977442	57	2e-08
gi	10067622	gb	AAE40379.1	Sequence 14 from patent US 6001580	56	3e-08
gi	12225888	emb	CAC21764.1	(AX048742) unnamed protein prod...	56	3e-08
gi	1831628	gb	AAB46082.1	Sequence 12 from patent US 559590...	56	3e-08
gi	6733345	emb	CAB69292.1	(A84425) unnamed protein product...	56	3e-08
gi	1831623	gb	AAB46077.1	Sequence 4 from patent US 5595904...	56	3e-08
gi	6733363	emb	CAB69301.1	(A84443) unnamed protein product...	56	3e-08
gi	11340599	emb	CAC17053.1	(AX041002) unnamed protein prod...	56	3e-08
gi	2830527	gb	AAC00731.1	I68405 Sequence 2 from patent US 5...	56	4e-08
gi	5985705	gb	AAE16513.1	Sequence 14 from patent US 5837853	56	4e-08
gi	5976242	gb	AAE13652.1	Sequence 6 from patent US 5830699...	55	6e-08
gi	6779545	emb	CAB70484.1	(A95607) unnamed protein product...	55	6e-08
gi	10051515	gb	AAE28422.1	Sequence 25 from patent US 5958784	54	1e-07
gi	2489140	gb	AAB77276.1	I57261 Sequence 13 from patent US ...	54	1e-07
gi	2830537	gb	AAC00741.1	I68415 Sequence 30 from patent US ...	54	1e-07
gi	10052141	gb	AAE29048.1	Sequence 6 from patent US 5962232	54	2e-07
gi	12813500	gb	AAE44800.1	Sequence 29 from patent US 6083713	54	2e-07
gi	10051526	gb	AAE28433.1	Sequence 36 from patent US 5958784	53	2e-07
gi	10051513	gb	AAE28420.1	Sequence 23 from patent US 5958784	53	3e-07
gi	2725137	gb	AAB92819.1	I67157 Sequence 25 from patent US ...	53	3e-07
gi	5944578	gb	AAE02654.1	Sequence 9 from patent US 5861300...	53	3e-07
gi	2489138	gb	AAB77274.1	I57259 Sequence 11 from patent US ...	52	3e-07
gi	10043358	emb	CAC07738.1	(AX019387) unnamed protein prod...	52	3e-07
gi	5976239	gb	AAE13649.1	Sequence 3 from patent US 5830699...	52	4e-07
gi	5942086	gb	AAE01618.1	Sequence 2 from patent US 5858765	52	4e-07
gi	6731333	emb	CAB69156.1	(A80507) unnamed protein product...	52	4e-07
gi	6001914	gb	AAE22876.1	Sequence 2 from patent US 5854392	52	5e-07
gi	12225880	emb	CAC21762.1	(AX048734) unnamed protein prod...	52	5e-07
gi	12225896	emb	CAC21766.1	(AX048750) unnamed protein prod...	52	5e-07
gi	12225920	emb	CAC21772.1	(AX048774) unnamed protein prod...	52	6e-07

Alignments

>gi|9928920|emb|CAC05182.1| (AX005954) unnamed protein product [Candida albicans]
Length = 339

Score = 624 bits (1609), Expect = e-179
Identities = 333/339 (98%), Positives = 335/339 (98%)

Query: 1 MKLSDYYIDKELIYNSAISDIYTAIDKFNNLPVCLKIVDEDFSLPPHSIHREIFILKTLK 60
MKLSDYYIDKELIYNSAISDIYTAIDKFNNLPVCLKIVDEDFSLPPHSIHRE+ ILKTLK
Sbjct: 1 MKLSDYYIDKELIYNSAISDIYTAIDKFNNLPVCLKIVDEDFSLPPHSIHREVLILKTLK 60

Query: 61 PHPNIIIEYFNDLKIYDDVILVTKLYRYDLSQLIEITKYCKRTRTFIYGINGNLVSNQYTL 120
PHPNIIIEYFNDLKI DD+ILVTKLYRYDLSQLIEITKYCKRTRTFIYGINGNLVSNQYTL
Sbjct: 61 PHPNIIIEYFNDLKICDDIILVTKLYRYDLSQLIEITKYCKRTRTFIYGINGNLVSNQYTL 120

Query: 121 ANEIEEKDIKLWLKSMSSGLEFIHSQGIHRDIKPSNIFFARDDITQPIIGDFDICYDLK 180
ANEIEEKDIKLWLKSMSSGLEFIHSQGIHRDIKPSNIFFARDDITQPIIGDFDICYDLK
Sbjct: 121 ANEIEEKDIKLWLKSMSSGLEFIHSQGIHRDIKPSNIFFARDDITQPIIGDFDICYDLK 180

Query: 181 LPPKDEPPMAKYIDVSTGIYKAPELILGITNYEYEIDIWSLGIILTGLYSENFQSVLVKD 240

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 Sbjct: 181 SPPKDEPPMAKYIDVSTGIYKAPELILGITNYEYEIDIWSLGIILTGLYSENFQSVLVKD 240

Query: 241 DKELTNDSHVSDLYLLNQIFENFGTPNLTD FEDELFCDEYNNENLHFKKFNLQKYPRKDW 300
 DKELTNDSHVSDLYLLNQIFENFGTPNLTD FEDELFCDEYNNENLHFKKFNLQKYPRKDW
 Sbjct: 241 DKELTNDSHVSDLYLLNQIFENFGTPNLTD FEDELFCDEYNNENLHFKKFNLQKYPRKDW 300

Query: 301 DIILPRCNDDLMKEIFTKMIRYDRSKRITSKEILQLMLD 339
 DIILPRCNDD MKEIFTKMIRYDRSKRITSKEILQLMLD
 Sbjct: 301 DIILPRCNDDFMKEIFTKMIRYDRSKRITSKEILQLMLD 339

>gi|6733419|emb|CAB69315.1| (A84499) unnamed protein product [unidentified]
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Score = 82.2 bits (202), Expect = 4e-16

Identities = 82/316 (25%), Positives = 141/316 (43%), Gaps = 54/316 (17%)

Query: 21 IYTAIDKFNNLPVCLKIV--DEDFSLPPHSIHREIFILKTLKPHPNIEYFNDLKIYDDV 78
 +Y A +K V LK + D + P + REI +LK L HPNI++ + + + +
 Sbjct: 264 VYKARNKLTGEVVALKKIRLDTETEGVPSTAIREISLLKELN-HPNIVKLLDVIHTENKL 322

Query: 79 ILVTKLYRYDLSQLIEITKYCKRTRFIYGINGNLVSNQYTLANEIEEKDIKLWLKSMSS 138
 LV + DL + ++ + + GI L IK +L +
 Sbjct: 323 YLVFEFLHQDLKKFMDASA-----LTGIPLPL-----IKSYLFQLLQ 359

Query: 139 GLEFIHSQGIHRDIKPSNIFFARDDITQPIIGDFDICYDLKLPPKDEPPMAKYIDVSTG 198
 GL F HS ++HRD+KP N+ + + + DF + +P + +V T
 Sbjct: 360 GLAFCHSHRVLHRDLKPQNLLINTEGAIK--LADFGGLARAFGVPVRTYTH-----EVVTL 412

Query: 199 IYKAPELILGITNYEYEIDIWSLGIILTGLYSENFQSVLVKDDKELTNDSHVSDLYLLNQ 258
 Y+APE++LG Y +DIWSLG I + +V DS + L+ +
 Sbjct: 413 WYRAPEILLGSKYYSTAVDIWSLGCIF-----AEMVTRRALFPGDSEIDQLF---R 460

Query: 259 IFENFGTPNLTD FEDELFCDEYNNENLHFKKFNLQKYPRKDWDIILPRCNDDLMKEIFTK 318
 IF GTP+ + +Y K + K+ R+D+ ++P ++D + + ++
 Sbjct: 461 IFRTLGTGPDEVVWPGVTSMPDY-----KPSFPKWARQDFSKVVPPLDED-GRSLLSQ 511

Query: 319 MIRYDRSKRITSKEIL 334
 M+ YD +KRI++K L
 Sbjct: 512 MLHYDPNKRISAKAAL 527

>gi|10061049|gb|AAE37002.1| Sequence 2 from patent US 5986055
 Length = 298

Score = 82.2 bits (202), Expect = 4e-16

Identities = 82/316 (25%), Positives = 141/316 (43%), Gaps = 54/316 (17%)

Query: 21 IYTAIDKFNNLPVCLKIV--DEDFSLPPHSIHREIFILKTLKPHPNIEYFNDLKIYDDV 78
 +Y A +K V LK + D + P + REI +LK L HPNI++ + + + +
 Sbjct: 18 VYKARNKLTGEVVALKKIRLDTETEGVPSTAIREISLLKELN-HPNIVKLLDVIHTENKL 76

Query: 79 ILVTKLYRYDLSQLIEITKYCKRTRFIYGINGNLVSNQYTLANEIEEKDIKLWLKSMSS 138
 LV + DL + ++ + + GI L IK +L +
 Sbjct: 77 YLVFEFLHQDLKKFMDASA-----LTGIPLPL-----IKSYLFQLLQ 113

Query: 139 GLEFIHSQGIHRDIKPSNIFFARDDITQPIIGDFDICYDLKLPPKDEPPMAKYIDVSTG 198
 GL F HS ++HRD+KP N+ + + + DF + +P + +V T
 Sbjct: 114 GLAFCHSHRVLHRDLKPQNLLINTEGAIK--LADFGGLARAFGVPVRTYTH-----EVVTL 166

Query: 199 IYKAPELILGITNYEYEIDIWSLGIILTGLYSENFQSVLVKDDKELTNDSHVSDLYLLNQ 258